

## DESTABILIZED BIOLUMINESCENT PROTEINS

### CROSS REFERENCE TO RELATED APPLICATIONS

The present application claims the priority of U.S. provisional patent application number  
5 60/463,851, entitled "Destabilized Lux," filed April 18, 2003. The foregoing is herein  
incorporated by reference in its entirety.

### STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

This invention was made with U.S. government support under grant number RO1 2580  
127 awarded by the Department of Energy. The U.S. government may have certain rights in the  
10 invention.

### FIELD OF THE INVENTION

The invention relates generally to the fields of molecular biology, microbiology, and  
micro-processing. More particularly, the invention relates to expression in prokaryotic and  
eukaryotic cells of genes encoding variants of bioluminescent proteins having shorter half lives.  
15 of luminescence than their wild-type counterparts.

### BACKGROUND

Bioluminescence refers to the production of light by a chemical reaction that originates in  
a living organism. Primarily a marine phenomenon, bioluminescence is observed in a broad  
variety of organisms ranging from bacteria to fish, crustaceans and squid, but is primarily  
20 attributable to chemical reactions that occur in bacteria and dinoflagellates. Among land  
dwelling organisms, bioluminescence is found among certain centipedes, millipedes and insects  
such as fireflies and click beetles but is unknown in plants, birds, reptiles, amphibians and  
mammals.

Genes responsible for the production of bioluminescent proteins have been isolated by  
25 molecular cloning techniques, leading to the widespread and expanding use of such proteins in a  
variety of applications including, *inter alia*, use as: 1) bioreporters for detection of environmental  
compounds, 2) reagentless components in bioelectronic devices, 3) whole cell logic gates for  
biocomputing, 4) tools for *in situ* functional imaging, 5) markers of recombinant strains released  
into the environment, and 6) markers to enable *in vivo* imaging of bacteria during systemic  
30 infection in animal hosts (Applegate et al., Appl. Environ. Microbiol., 64:2730-2735, 1998;

Sayler, G.S., and Ripp, S., Current Opinion in Biotechnology, 11:286-289, 2000; and Liu et al., Plasmid, 44:250-261, 2000).

Luciferases of the lux family (Lux) are bioluminescent proteins derived from certain bioluminescent bacterial strains that have found widespread use in various applications. Lux is the product of the *luxAB* genes, which encode luciferase, a heterodimeric bioluminescent catalyzing enzyme. The entire *luxCDABE* cassette has been isolated from several bioluminescent bacteria including *Vibrio fischeri*, *V. harveyi*, and *Photobacterium luminescens*. Use of the complete operon of bacterial luciferase (i.e., *luxCDABE*) has enabled construction of self-sufficient bioreporters containing all of the required elements for production of light in response to specific chemicals or physical agents.

Despite these considerable advances, currently available bioreporters based on *luxCDABE* are not ideally suited for applications requiring a relatively short half life of the reporter protein. As one example, the duration of Lux emission by existing bioreporters limits their usefulness for monitoring certain events in real time, such as both initiation and termination of transcription in a cell. Additionally, in applications using bioreporters in synthetic gene circuits, the long time constants associated with decay of presently available reporter proteins can significantly degrade circuit performance.

## SUMMARY

The invention relates to modified *lux*-based nucleic acid and vector compositions as well as bioreporter cells, both prokaryotic and eukaryotic, incorporating these compositions. The modified Lux proteins emit bioluminescence with a duration shorter than that of conventional

5 *lux*-based bioreporters. More specifically, the bioreporters are engineered to express variants of LuxA and LuxB proteins that are rapidly degradable via cellular proteolytic pathways and mechanisms, such as by tail-specific proteases in bacterial cells and by a ubiquitin-proteasome pathway in eukaryotic cells. Degradation of the modified bioluminescent proteins reduces the duration of the bioluminescent response produced upon stimulation by an effector molecule.

10 This feature is advantageous for a wide variety of real-time or temporally responsive biosensing, biocomputing, and Lux array technologies.

Accordingly, in one aspect the invention includes a purified nucleic acid construct including a gene cassette encoding at least one modified bioluminescent protein. The modified protein can contain at least one modification in its amino acid sequence relative to the sequences

15 of an unmodified form of the same protein, wherein the modification includes the addition of a peptide sequence to the protein. The addition of the peptide sequence reduces a first duration of bioluminescence emitted by the modified bioluminescent protein relative to a second duration of bioluminescence emitted by the unmodified form of the protein.

In preferred embodiments of the purified nucleic acid construct, the gene cassette

20 encodes a luciferase protein. The luciferase protein can include at least one a Lux protein selected from Lux A and Lux B. The Lux protein can include the amino acid sequence of a Lux protein isolated from bacterial strains including *Photorhabdus luminescens*, *Vibrio fischeri* and *Vibrio harveyi*.

In some versions of the nucleic acid, the gene cassette can encode all proteins necessary

25 for production of bioluminescence without addition of an exogenous substrate. For example, the purified nucleic acid construct can include a lux CDABE cassette. Other versions of the cassette requiring addition of exogenous substrate can include, for example, only a bioluminescent protein such as luciferase.

The modified form of the bioluminescent protein encoded by the nucleic acid of the

30 invention can include the addition of a peptide sequence that specifically binds to a protein associated with a proteolytic pathway.

The protein associated with a proteolytic pathway can be a tail-specific protease. In particular embodiments based on tail-specific proteases, the peptide sequence of the modified bioluminescent protein can include the amino acid sequences of SEQ ID NOS:8-10. In particular embodiments using Lux proteins, these peptide sequences can be added to one or both of LuxA and Lux B.

In other versions of the nucleic acids of the invention, the protein associated with a proteolytic pathway can be one that mediates degradation of the modified bioluminescent protein via a ubiquitin-proteasome pathway. The protein that mediates degradation via this pathway can be SCF(Grr1). In a preferred embodiment utilizing this pathway, the peptide sequence of the modified bioluminescent protein can include a PEST-rich sequence. The PEST-rich sequence can be a carboxy terminus of G1 cyclin (*Cln2*).

Another aspect of the invention is a vector including a gene cassette encoding at least one modified bioluminescent protein. The modified protein can contain at least one modification in its amino acid sequence relative to the sequence of an unmodified form of the same protein, wherein the modification includes the addition of a peptide sequence to the protein. The addition of the peptide sequence reduces a first duration of bioluminescence emitted by the modified bioluminescent protein relative to a second duration of bioluminescence emitted the unmodified form of said protein.

The vector can be a plasmid.

The vector can be an expression vector suitable for driving expression in a cell type such as a bacterial cell, a yeast cell or a mammalian cell.

Yet a further aspect of the invention is a cell expressing the vector of the invention. The cell can be a prokaryotic cell, for example a bacterial cell. Preferred embodiments of the prokaryotic cells harbor a vector that includes the purified nucleic acid of claim 7 or 8.

The cell can also be a eukaryotic cell such as a yeast cell or a mammalian cell.

The modification in the purified nucleic acid reduces a first duration of bioluminescence emitted by the modified protein relative to a second duration of bioluminescence emitted by the unmodified protein. The duration of bioluminescence can be determined by comparing a time course of a first measure of bioluminescence emitted by the modified protein and a time course of a second measure of bioluminescence emitted by the unmodified protein. The first measure can be between about 100-fold and 1000-fold lower than the second measure.

Unless otherwise defined, all technical terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are  
5 incorporated by reference for the proposition cited. In the case of conflict, the present specification, including any definitions will control. The particular embodiments discussed below are illustrative only and not intended to be limiting.

The term "bioreporter," as used herein, refers to a biological system or organism that has  
10 been adapted or engineered to produce a detectable response in the presence of a selected compound or condition.

As used herein, "luminescence" refers to the production and/or emission of light by a chemical or electrical process, but not from a thermal source such as incandescence.

The terms "bioluminescence," "bioluminescent," and "bioluminesce" refer to  
15 luminescence that occurs in a living organism, for example in a photogenic organism, in which energy from a chemical reaction is transformed into light energy. An example of a bioluminescent chemical reaction is a reaction in which a chemical substrate such as luciferin reacts with oxygen in the presence of an enzyme; for example luciferase. "Bioluminescence," "bioluminescent," and "bioluminesce" also refer to the production of light using chemical  
20 reagents and reactions that produce bioluminescence in nature, in other contexts. As an example, bioluminescence may occur *in vitro*, or in a recombinant organism engineered to contain the chemical reagents necessary for bioluminescence in a naturally occurring organism.

"Fluorescence," as defined herein, refers to luminescence in the form of secondary light that is generated upon exposure to a primary light source. A substance emits light by  
25 "fluorescence" when it absorbs incident radiation at a first (i.e., excitation) wavelength and emits radiation at a second, usually different (i.e., emission) wavelength. Fluorescent emission ceases when the incident radiation ends. Accordingly, the mechanism of production of light by "bioluminescence" is distinct from the mechanism of production of light by "fluorescence."

The terms "LuxCDABE" and "LuxCDABE cassette" refer to an operon containing five  
30 genes necessary for self-sustained bioluminescence in bacteria. LuxAB is a luciferase which catalyzes the light-producing reaction. LuxCE is a multi-component enzyme that converts

myristic acid to a fatty aldehyde substrate for the light-producing reaction, with the assistance of a transferase, i.e., LuxD.

5 A "proteolytic pathway," as used herein, refers to a series of enzymatic or chemical steps by which a protein can be degraded in a cell into its constituent parts by one or more proteolytic enzymes.

The term "tail specific protease" refers to a class of proteolytic enzymes that recognize non-polar amino acid residues in the carboxy terminal end of another protein, and catalyze the degradation of the protein.

10 A "ubiquitin-proteasome pathway," as herein defined refers to a series of steps leading to degradation within a cell of a protein containing a PEST sequence that is recognized and ubiquitinated, thereby marking it for degradation by a proteasome. The term "proteasome," as used herein, refers to an ATP-dependent multi-enzyme complex, variably composed of several subunits and located within the cytoplasm and/or nucleus of a cell, that is involved in selective protein degradation.

15 The term "vector," as used herein refers a vehicle used for the introduction of a nucleic acid, such as a recombinant DNA molecule, into a host. A vector may be a plasmid, a transposon, a virus, or any other suitable vehicle. An "expression vector" refers to a vector containing a nucleic acid, for example a DNA molecule encoding a gene product of interest, and further including regulatory elements useful for the expression of a gene product in a host, including but not limited to a promoter and a termination sequence.

20 Other features and advantages of the invention will be apparent from the following detailed description, and from the claims.

## BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a graph showing changes in bioluminescence over time, in transformed *E. coli* cells following various periods of inhibition of transcription and translation.

FIG. 2 is a graph showing expansion of the data in FIG. 1, illustrating bioluminescent  
5 behavior of constructs producing lower levels of light.

FIG. 3 is a graph showing a comparison of relative bioluminescence over time of Lux variants AaavB and AaavBaav.

## DETAILED DESCRIPTION

The invention relates to purified nucleic acid constructs that include a gene cassette encoding at least one modified bioluminescent protein. The modified protein contains a modification in its amino acid sequence, relative to the sequence of an unmodified form of the same protein, that causes the duration of bioluminescence emitted by the modified protein to be shorter than the duration of bioluminescence emitted by an unmodified form of the same protein.

### Biological Methods

Methods involving conventional molecular biology techniques are described herein.

Such techniques are generally known in the art and are described in detail in methodology treatises such as *Molecular Cloning: A Laboratory Manual*, 3<sup>rd</sup> ed., vol. 1-3, ed. Sambrook et al., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 2001; and *Current Protocols in Molecular Biology*, ed. Ausubel et al., Greene Publishing and Wiley-Interscience, New York, 1992 (with periodic updates). Methods for chemical synthesis of nucleic acids are discussed, for example, in Beaucage and Carruthers, *Tetra. Letts.* 22:1859-1862, 1981, and Matteucci et al., *J. Am. Chem. Soc.* 103:3185, 1981. Chemical synthesis of nucleic acids can be performed, for example, on commercial automated oligonucleotide synthesizers.

Methods involving conventional biology and microbiology are also described herein.

Such techniques are generally known in the art and are described in detail in methodology treatises such as Sambrook et al., *supra*; *Current Protocols in Molecular Biology*, ed. Ausubel et al., Greene Publishing and Wiley-Interscience, New York, 1992 (with periodic updates); *Techniques in Microbial Ecology*, ed. Robert S. Burlage et al., Oxford University Press, New York, NY, 1998; *Environmental Microbiology*, ed. Raina M. Maier, Academic Press, Burlington, MA, 2000; and *Environmental Molecular Microbiology: Protocols and Applications*, ed. Paul. A Rochelle, Bios Scientific Publishing, Ltd., Oxford, UK, 2001. Methods involving culturing and manipulation of yeast cells are described in *Methods In Yeast Genetics: A Cold Spring Harbor Laboratory Course Manual*, 2002, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. Methods for measuring bioluminescence, for example using a luminometer, are well known in art and are generally described in treatises such as *Physical Optics and Light Measurements (Methods of Experimental Physics)*, Vol. 26, 1989, Daniel Malacara, ed., Academic Press.



## Modified Bioluminescent Proteins

Modified bioluminescent proteins encompassed by the invention include any bioluminescent protein modified in such a way as to emit bioluminescence of shorter duration than that of the corresponding unmodified ("native" or "wild type") protein. The modification includes the addition of a peptide sequence to the amino acid sequence of the protein. Addition of the peptide reduces the duration of bioluminescence emitted by the modified bioluminescent protein, relative the duration of bioluminescence emitted by the same protein in unmodified form. The reduction in duration of bioluminescence can be determined, for example, by comparing a time course of a first measure of bioluminescence emitted by the modified protein with that of a second measure of bioluminescence emitted by the unmodified protein. The first measure can be between about 100-fold and 1000-fold, (i.e., about 200, 300, 400, 500, 600, 700, 800, 900, and 1000-fold) lower than the second measure of bioluminescence emitted by the unmodified form of the protein.

Those of skill in the arts of molecular and cellular biology will recognize that many schemes may be utilized to produce such a modified bioluminescent protein. One scheme for shortening the duration of the bioluminescent response is to reduce the overall numbers of bioluminescent protein molecules present in a cell at a given time by "destabilizing" these molecules, for example by targeting them for degradation within the cell. According to the foregoing strategy, one preferred embodiment of a modified bioluminescent protein of the invention is one in which the amino acid sequence of the modified protein includes a peptide that specifically binds to a protein associated with a proteolytic pathway that targets the modified protein for degradation.

The choice of cellular proteolytic pathway can be guided by the type of cell in which the bioreporter is constructed. For example, an exemplary proteolytic pathway in a bacterial cell involves the action of a class of enzymes termed "tail-specific proteases" (TSP) present in *Escherichia coli* and other gram-negative species (Silber KR et al., 1992, Proc Natl Acad Sci USA 89, 295-299; Keiler KC et al. Science 1996, 271:990-993; Keiler KC and Sauer RT J. Biol Chem 1996, 2589-2593). TSP enzymes catalyze the proteolysis of proteins containing certain peptide sequences in their carboxyl termini (tails) by specifically binding to those sequences, facilitating degradation of the bound protein by the protease. A naturally occurring protein degradation system in a bacterial cell, such as TSP, can therefore be exploited to degrade

modified proteins in which a peptide sequence recognized by the enzyme has been incorporated into the amino acid sequence of the modified protein (Andersen, JB et al., Appl. Environ Microbiol 1998, 2240-2246; Elowitz, MB and S Leibler 2000. Nature 403:335-338).

In accordance with the above scheme for degradation of modified bioluminescent proteins, some embodiments of the modified bioluminescent proteins of the invention incorporate into the amino acid sequence of the protein a carboxyl-terminal tag recognized by a TSP enzyme. Specific examples of such proteins are described in examples below, and include modified versions of the bacterial luciferase holoenzyme LuxAB. Short half-life variants of LuxA and LuxB, along with a double-modified variant were constructed and cloned into *E. coli*.

Results of bioluminescence assays using transfected bacterial cells indicated that the addition of a carboxy-terminal tag decreased the functional half-life of the holoenzyme. In some embodiments of the modified bioluminescent proteins of the invention, the amino acid sequence of the protein includes peptides having sequences listed herein as SEQ ID NOS:8-10.

An exemplary proteolytic pathway that can be utilized in a eukaryotic cell, such as a yeast cell or a mammalian cell, is the ubiquitin-proteasome pathway. Degradation of proteins by this pathway in a mammalian cell, utilizing a motif known as "PEST," is described, for example, in Li X et al. 1998 J Biol Chem 273:34970-75. The ubiquitin-proteasome pathway in yeast is described, for example, in Berset C et al., Mol. Cell Biol 2002, 13:4463-76. Analyses of the molecular components of this pathway have led to the elucidation of a domain within the G1 cyclin Cln2 (PEST motif) that is recognized by a component of the ubiquitin-ligase complex within yeast cells, i.e., SCF(Grr1). Binding of the Cln2 domain to SCF(Grr1) causes a protein containing the Cln2 domain to be targeted for destruction by the ubiquitin-proteasome pathway. Accordingly, incorporation of a PEST-rich domain into a modified bioluminescent protein of the invention can target the modified protein for degradation by the ubiquitin-proteasome pathway. Methods for selecting particular PEST sequences useful for addition as "degradation domain" peptides are discussed, for example, in Li et al., *supra*, and in Mateus C and Avery SV, Yeast 2000, 16:1313-23. Embodiments of modified bioluminescent proteins based on utilization of the ubiquitin-proteasome pathway are further described in examples below.

Nucleic Acids, Vectors and Cells Including Constructs Encoding

Modified Bioluminescent Proteins

The invention further pertains to nucleic acid-based compositions including purified nucleic acids that encode the above-described modified bioluminescent proteins, vectors that incorporate these nucleic acids, and cells transformed with these vectors, causing the cells to express the modified proteins. Accordingly, one aspect of the invention is a purified nucleic acid construct that includes a gene cassette encoding at least one modified bioluminescent protein. The modified protein contains a modification in its amino acid sequence relative to the sequence of an unmodified form of the same protein, wherein the modification causes the duration of bioluminescence emitted by the modified protein to be shorter than the duration of bioluminescence emitted by an unmodified (wild-type) form of said protein. As described above, in preferred embodiments, the modifications involve additions (such as carboxyl tags) to the amino sequences of the proteins. Accordingly, the nucleic acids of the invention include those that encode the bioluminescent proteins modified to include such additional sequences.

General methods of making the various embodiments of the nucleic acid constructs of the invention in both prokaryotic cells (i.e., bacteria) and eukaryotic cells (i.e., yeast) are well known in the art of molecular biology. Specific examples related to modified Lux A and Lux B variants are described in detail in the examples below, and various starting materials are listed in Tables 1 and 2 *infra*.

Vectors of use in the invention are any that can be used to drive expression of the gene cassette of interest in an appropriate cell type. Many types of suitable vectors are commercially available and are well known to those of skill in the art of molecular biology. Examples of specific vectors that can be used in the practice of the invention are further described in the below examples.

## EXAMPLES

The present invention is further illustrated by the following specific examples, which should not be construed as limiting the scope or content of the invention in any way.

### Example 1-Materials and Methods for Construction of Destabilized Lux

5 Genetic constructs. Primers used in construction of the *Lux* variants are shown in Table 1. Wild type and modified variants of the *luxA* and *B* genes were amplified by PCR directly from *P. luminecens* genomic DNA (ATCC Accession No. 29999).

**Table 1. Primers used in construction of *Lux* variants**

10	<i>KpnI</i>	Start
	LuxA forward: 5'- <u>GGTACC</u> GC ATG AAA TTT GGA AAC TTT TTG -3'	
	(SEQ ID NO:1)	
15	<i>XmaI</i>	Start
	LuxB forward: 5'- <u>CCCGGG</u> CT AAG GAG AAA GAA ATG AAA.T.-3'	
	(SEQ ID NO:2)	
20	<i>BamHI</i>	Stop
	LuxB reverse: 5'- TTA <u>GGATCC</u> TA TTA G GTA TAT TCC ATG TGG TAC TTC -3'	
	(SEQ ID NO: 3)	
25	<i>XmaI</i>	Stop V A A
	LuxAaav reverse: 5'-TTA <u>CCCGGG</u> A CTA AAC TGC TGC AGC GTA GTT TTC GTC GTT	
	TGC TGC AGG CCT ATA TAA TAG CGA ACG TTG TTT -3'	
	(SEQ ID NO:4)	
30	<i>XmaI</i>	Stop A A L
	LuxAlaa reverse: 5'-TTA <u>CCCGGG</u> A CTA AGC TGC TAA AGC GTA GTT TTC GTC GTT	
	TGC TGC AGG CCT ATA TAA TAG CGA ACG TTG TTT -3'	
	(SEQ ID NO:5)	
35	<i>XmaI</i>	Stop V S A
	LuxAasv reverse: 5'-TTA <u>CCCGGG</u> A CTA AAC TGA TGC AGC GTA GTT TTC GTC GTT	
	TGC TGC AGG CCT ATA TAA TAG CGA ACG TTG TTT -3'	
	(SEQ ID NO:6)	
40	<i>BamHI</i>	Stop V A A
	LuxBaav reverse: 5'-TTA <u>GGATCC</u> TA TTA AAC TGC TGC AGC GTA GTT TTC GTC GTT	
	TGC TGC AGG ACT GGT ATA TTC C ATG TGG TAC TTC -3'	
	(SEQ ID NO:7)	

Unique restriction sites used in the final assembly are underlined. Start and stop codons and pertinent amino acids are indicated above the respective sequences.

5 Bacterial strains and plasmids used in the construction of the *Lux* variants are shown in Table 2.

**Table 2: Strains and plasmids used to construct *Lux* fusions**

10	Name	Properties	Source
	<i>Escherichia coli</i> TOP10	Cloning and expression strain	Invitrogen (Carlsbad,CA)
15	pCR2.1	Am <sup>R</sup> , Km <sup>R</sup>	Invitrogen
	pZE21-GFPaav	Km <sup>r</sup> ; GFP-reporter plasmid. All subsequent plasmids used in this study were derived from this plasmid with the GFPaav removed and replaced with <i>luxA</i> and/or <i>luxB</i> variants.	Elowitz and Liebler
20	pAB	pZE21 with the wild-type <i>luxAB</i> of <i>P. luminescens</i> cloned in place of <i>GFPaav</i> .	This work
25	pAaavB	pZE21 containing the <i>luxA</i> gene modified to include the gene sequence of the 11-amino acid carboxy-terminal tag AANDENYAAAV (SEQ ID NO:8), and the wild type <i>luxB</i> . Estimated $t_{1/2}$ = 60min.	This work
30	pAlaaB	pZE21 containing the <i>luxA</i> gene modified to include the gene sequence of the 11-amino acid carboxy-terminal tag AANDENYALAA (SEQ ID NO:9), and the wild type <i>luxB</i> . Estimated $t_{1/2}$ = 40min.	This work
35	pAasvB	pZE21 containing the <i>luxA</i> gene modified to include the gene sequence of the 11-amino acid carboxy-terminal tag AANDENYAASV (SEQ ID NO:10), and the wild type <i>luxB</i> . Estimated $t_{1/2}$ = 110min.	This work
40	pABaav	pZE21 containing the <i>luxB</i> gene modified to include the gene sequence of the 11-amino acid carboxy-terminal tag AANDENYAAAV (SEQ ID NO:8), and the wild type <i>luxA</i> . Estimated $t_{1/2}$ = 60min.	This work
45	pAaavBaav {WP176642;1}	pZE21 containing the <i>luxA</i> and <i>luxB</i> genes modified	This work

to include the gene sequence of the 11-amino acid  
carboxy-terminal tag AANDENYAAAV (SEQ ID NO:8).

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5 Wild type luxAB and luxABaav were amplified by PCR, gel purified, and cloned into the  
TOPO-TA cloning vector pCR2.1 (Invitrogen, Carlsbad, CA) according to the manufacturer's  
instructions.

For production of luxA variants, luxBaav, and wild-type luxB, the genes were  
independently amplified and cloned. The luxA variants were digested overnight with XmaI and  
10 XbaI and ligated upstream of the luxB or luxBaav genes in plasmid pCR2.1. The wild type  
luxAB and the newly assembled variants were then each digested overnight from their respective  
TA-cloning vectors with BamHI and KpnI, gel purified, and directionally cloned in place of the  
GFPaav gene of the repressilator reporter plasmid (Elowitz MB and Leibler S 2000. Nature  
403:335-338). T4 DNA ligase was purchased from Fisher Scientific (Pittsburgh, PA), and all  
15 other enzymes were purchased from Promega (Madison, WI).

#### Example 2- Assay of Bioluminescence

Overnight cultures of the four *Lux* variants and a negative control carrying the parent  
vector with the gene for green fluorescent protein (GFP) were transferred into triplicate tubes of  
fresh LB medium containing 50 ug/mL kanamycin. Cultures were then grown to an optical  
20 density at 546 nm ( $OD_{546}$ ) of ~ 0.6. Bioluminescence measurements were made at  $t=0$  as  
described below. Subsequently, rifampicin (150  $\mu$ g/mL) and tetracycline (30  $\mu$ g/mL) were  
added to all cultures to block transcription and translation, respectively.

For bioluminescence measurements, samples of one mL volume were taken immediately  
( $t=0$ ) and at 30 min. intervals thereafter and assayed for  $OD_{546}$  and bioluminescence.  $OD_{546}$  was  
25 measured in a Beckman DU-640B spectrophotometer. Bioluminescence was assayed by first  
adding 10  $\mu$ L of N-decanal (Sigma, St. Louis, MO) to the 1-mL samples, inverting 10 times, and  
measuring light with a SDI Deltatox handheld luminometer. Some assays were conducted with  
addition of bacteriostatic antibiotics to block transcription and translation (rifampicin and  
tetracycline, respectively), followed by monitoring bioluminescence in the presence of aldehyde  
30 over time. Three light measurements were taken in rapid succession and these values were  
averaged for each sample. Standard deviations between the averages of three independent  
samples were calculated.

### Example 3- Lux-based Bacterial Bioreporters Exhibiting Reduced Bioluminescent Half Life

Bioluminescence measurements were compared in *E. coli* strains harboring plasmids containing the wild type *luxAB* genes of *P. luminescens* (Meighen EA 1991 Microbiological Reviews 55:123-142) behind a constitutive promoter, and those containing *luxA* and *luxB* variants containing carboxy-terminal tags constructed as described above.

Referring to FIG. 1, the results showed that inhibition of transcription or translation resulted in a rapid decline in bioluminescence within 30 minutes ( $t_{1/2}$ ) in cells expressing wild-type *luxA* (FIG. 1, pAB). The maximum bioluminescence at times  $t=0$  are consistent with the quantity of luciferase expected to accumulate within the cells when being constitutively expressed. Luciferase with a short half-life does not accumulate to the same level as the wild-type, the decreases in half-life resulting in lower levels of bioluminescence at  $t=0$ .

Modification of the LuxA protein by addition of the -aav tag to the *luxA* gene resulted in an approximate 100-fold decrease in bioluminescence at time  $t_0$  (pAaavB in FIG. 1). An even more dramatic decrease in initial bioluminescence was observed when both LuxA and LuxB included the -aav tag (FIG. 1, pAaavBaav). The double modified holoenzyme produced bioluminescence nearly 1000-fold less than that of the wild type. (FIG. 1 and 2). Unexpectedly, modification of the LuxB monomer alone (pABaav) did not result in decreased bioluminescence over time and did not decrease peak bioluminescence. Bioluminescence in this variant was found to be similar to that of the wild type (pAB) over the course of the experiments (FIG. 1).

FIG. 3 shows results from a separate assay in which bioluminescence was compared in the single and double variants of LuxB, i.e., pAaavB and pAaavBaav. The result shows that the behavior of the bioluminescent curve drops measurably over time for both variants, and that the rate of decline is consistent with the expected half-life of the variants.

To determine if the drop in bioluminescence output could be attributed to interference of enzymatic activity by the carboxy-terminal tag, two additional constructs were made with predicted half-lives either greater (i.e., -asv tag; 110 min.) or lesser (i.e., -laa tag; 40 min.) than those predicted for -aav tag (60 min.). The predicted half lives of these variants are also indicated in Table 2, *supra*. The results showed that *E. coli* containing pAasvB resulted in bioluminescence values higher than that of pAaavB ( $3.35 \times 10^5$  vs.  $1.3 \times 10^4$ , respectively), and one third of that produced by the wild-type holoenzyme ( $1.0 \times 10^6$ ). *E. coli* harboring pAlaaB

resulted in bioluminescence measurements lower than that produced with pAaavB (i.e.,  $7.2 \times 10^3$  vs.  $1.3 \times 10^4$ , respectively), consistent with the predicted results listed in Table 2.

The results for variants containing the modified *luxA* genes thus indicated that: 1) a single modification of this monomer is sufficient to result in decreased half-life of the heterodimeric holoenzyme, and 2) half-life of the holoenzyme can be fine-tuned in an application-specific manner by incorporating different carboxy-terminal tags. Modification of both subunits resulted in decreased peak bioluminescence, but did not dramatically affect the half-life of the holoenzyme. Unexpectedly, modification of the LuxB monomer alone neither decreased peak bioluminescence nor resulted in decreased bioluminescence over time.

#### Example 4- Methods For Construction of Lux-based Eukaryotic Bioreporter in Yeast

This example describes the construction of bioreporters in yeast cells that exhibit a reduced half life of lux-based bioluminescence relative to control bioreporters. Reduction of the half life is based on degradation of the modified bioluminescent protein by the ubiquitin-proteasome pathway.

Genetic constructs. Using modifications of methods described above, the PEST-rich 178 carboxy terminus (C-terminus) of the G1 cyclin Cln2 (described in Berset et al., Mol. Cell Biol. 22:4463-4476, 2002; and Salama et al., Mol. Cell Biol. 14:7953-7966, 1994) was fused to the C-terminus of the *Pseudomonas luminescens luxA* and *luxB* genes that encode the heterodimeric luciferase (Lux AB) protein, to form modified *lux A* (i.e., *luxAcln*) and *lux B* (i.e., *luxBcln*) genes. The fused DNA sequences were cloned into a suitable yeast expression vector (i.e., pBEV-Y), described by Miller CA et al. 1998 *Nucleic Acids Res.* 26:3577–3583.

Bioluminescent yeast strains. Yeast cells (*Saccharomyes cerevisiae*) were transformed with constructs containing wild-type and the modified *luxA* and *luxB* genes along with the a plasmid containing *luxC*, *luxD*, *luxE* and *frp* genes. Plasmids used in this work, including pLCIRESDEIRESfrp, pUA12B7 and pGUA9B19 are described in Gupta et al. FEMS Yeast Research 4:305-313). These transformations generated *S. cerevisiae* strains able to autonomously bioluminesce.

#### Example 5 – Lux-based Eukaryotic Bioreporters Exhibiting Reduced Bioluminescent Half Life

The characteristics of bioluminescence emitted by transformed yeast cells constructed as described above were tested using a bioluminescence assay. In cells expressing wild-type *luxA* and *luxBcln*, inhibition of protein synthesis with the antibiotic cycloheximide led to a rapid



decline in bioluminescence within 30 minutes ( $t_{1/2}$ ). By contrast, the duration of bioluminescence emitted by cells expressing wild-type *luxA* and *luxB* was much longer ( $t_{1/2}$  = 6 hours). Constructs containing *luxAcln* and the wild-type *luxB* did not show a significant rate of decline in bioluminescence. These data indicate that a modification of the *luxB* is sufficient to decrease the half-life of the bioluminescent reaction utilizing this tag.

#### Other Embodiments

This description has been by way of example of how the compositions and methods of the invention can be made and carried out. Various details may be modified in arriving at the other detailed embodiments, and many of these embodiments will come within the scope of the invention. For example, destabilized bioluminescent proteins may be expressed in eukaryotic cells other than yeast cells such as mammalian cells. Therefore, to apprise the public of the scope of the invention and the embodiments covered by the invention, the following claims are made.

What is claimed is: